

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Soos, Jeanne M.
Schiffenbauer, Joel
Johnson, Howard M.

10 (ii) TITLE OF INVENTION: Orally-Administered Interferon-Tau
Compositions and Methods

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Dehlinger & Associates
(B) STREET: 350 Cambridge Ave., Suite 250
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
20 (F) ZIP: 94306

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER:
(B) FILING DATE: 15-MAR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Sholtz, Charles K.
(B) REGISTRATION NUMBER: 38,615
(C) REFERENCE/DOCKET NUMBER: 5600-0003

(ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 415-324-0880
(B) TELEFAX: 415-324-0960

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ovis aries
- (B) STRAIN: Domestic
- (D) DEVELOPMENTAL STAGE: Blastula (blastocyst)
- (F) TISSUE TYPE: Trophectoderm
- (G) CELL TYPE: Mononuclear trophectoderm cells

(vii) IMMEDIATE SOURCE:

- (B) CLONE: oTP-1a

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..516

~~(x) PUBLICATION INFORMATION:~~

(A) AUTHORS: Ott, Troy L

Van Heeke, Gino

Johnson, Howard M

Bazer, Fuller W

(B) TITLE: Cloning and Expression in Saccharomyces

cerevisiae of a Synthetic Gene for the Type I

Trophoblast Interferon Ovine Trophoblast

Protein-1: Purification and Antiviral Activity

(C) JOURNAL: J. Interferon Res.

(D) VOLUME: 11

(F) PAGES: 357-364

(G) DATE: 1991

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	TGC TAC CTG TCG CGA AAA CTG ATG CTG GAC GCT CGA GAA AAT TTA AAA	48
	Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys	
5	1 5 10 15	
	CTG CTG GAC CGT ATG AAT CGA TTG TCT CCG CAC AGC TGC CTG CAA GAC	96
	Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp	
	20 25 30	
10	CGG AAA GAC TTC GGT CTG CCG CAG GAA ATG GTT GAA GGT GAC CAA CTG	144
	Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu	
	35 40 45	
15	CAA AAA GAC CAA GCT TTC CCG GTA CTG TAT GAA ATG CTG CAG CAG TCT	192
	Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser	
	50 55 60	
	TTC AAC CTG TTC TAC ACT GAA CAT TCT TCG GCC GCT TGG GAC ACT ACT	240
	Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	
	65 70 75 80	
	CTT CTA GAA CAA CTG TGC ACT GGT CTG CAA CAG CAA CTG GAC CAT CTG	288
	Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu	
	85 90 95	
	GAC ACT TGC CGT GGC CAG GTT ATG GGT GAA GAA GAC TCT GAA CTG GGT	336
	Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly	
	100 105 110	
30	AAC ATG GAT CCG ATC GTT ACT GTT AAA AAA TAT TTC CAG GGT ATC TAC	384
	Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr	
	115 120 125	
35	GAC TAC CTG CAG GAA AAA GGT TAC TCT GAC TGC GCT TGG GAA ATC GTA	432
	Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val	
	130 135 140	
	CGC GTT GAA ATG ATG CGG GCC CTG ACT GTG TCG ACT ACT CTG CAA AAA	480
40	Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys	
	145 150 155 160	
	CGG TTA ACT AAA ATG GGT GGT GAC CTG AAT TCT CCG	516

Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
165 170

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of a mature
OvIFNtau protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys	Tyr	Leu	Ser	Arg	Lys	Leu	Met	Leu	Asp	Ala	Arg	Glu	Asn	Leu	Lys	1	5	10	15
Leu	Leu	Asp	Arg	Met	Asn	Arg	Leu	Ser	Pro	His	Ser	Cys	Leu	Gln	Asp	20	25	30	
Arg	Lys	Asp	Phe	Gly	Leu	Pro	Gln	Glu	Met	Val	Glu	Gly	Asp	Gln	Leu	35	40	45	
Gln	Lys	Asp	Gln	Ala	Phe	Pro	Val	Leu	Tyr	Glu	Met	Leu	Gln	Gln	Ser	50	55	60	
Phe	Asn	Leu	Phe	Tyr	Thr	Glu	His	Ser	Ser	Ala	Ala	Trp	Asp	Thr	Thr	65	70	75	80
Leu	Leu	Glu	Gln	Leu	Cys	Thr	Gly	Leu	Gln	Gln	Gln	Leu	Asp	His	Leu	85	90	95	
Asp	Thr	Cys	Arg	Gly	Gln	Val	Met	Gly	Glu	Glu	Asp	Ser	Glu	Leu	Gly	100	105	110	
Asn	Met	Asp	Pro	Ile	Val	Thr	Val	Lys	Lys	Tyr	Phe	Gln	Gly	Ile	Tyr	115	120	125	
Asp	Tyr	Leu	Gln	Glu	Lys	Gly	Tyr	Ser	Asp	Cys	Ala	Trp	Glu	Ile	Val				

130

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Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
 145 150 155 160

5

Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
 165 170

10 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: synthetic nucleotide sequence encoding
 a mature human interferon-tau protein, HuIFNtaul.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTGACTTGT CTCAAAACCA CGTTTTGGTT GGTAGAAAGA ACTTAAGACT ACTAGACGAA 60

ATGAGACGTC TATCTCCACG CTTCTGTCTA CAAGACAGAA AGGACTTCGC TTTGCCTCAG 120

30 GAAATGGTTG AAGGTGGCCA ACTACAAGAA GCTCAAGCGA TATCTGTTTT GCACGAAATG 180

TTGCAACAAA GCTTCAACTT GTTCCACACC GAACACTCTT CGGCCGCTTG GGACACCACC 240

TTGTTGGAAC AGCTCAGAAC CGGTTTGCAC CAACAATTGG ACAACTTGGA TGCATGTTTG 300

35 GGTCAAGTTA TGGGTGAAGA AGACTCTGCT CTCGGGAGAA CCGGTCCAAC GCTAGCTTTG 360

AAGAGATACT TCCAAGGTAT CCACGTTTAC TTGAAGGAAA AGGGTTACTC TGACTGTGCT 420

40 TGGGAAACCG TGCCTCTAGA AATCATGCGT AGCTTCTCTT CTTTGATCAG CTTGCAAGAA 480

AGATTACGTA TGATGGACGG TGACTTGTCG AGCCCA 516

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence for a mature
HuIFNtau protein, HuIFNtau1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg
1 5 10 15
Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp
20 25 30
Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu
35 40 45
Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
50 55 60
Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
65 70 75 80
Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu
85 90 95
Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu Gly
100 105 110
Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His
115 120 125
Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val
130 135 140

Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu
 145 150 155 160

Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
 5 165 170

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau3, mature no leader sequence

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

30	TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGC CAG AAC CTC AGG	48
	Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg	
	1 5 10 15	
	CTC CTG GGC CAA ATG AGG AGA CTC TCC CTT CGC TTC TGT CTG CAG GAC	96
35	Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp	
	20 25 30	
	AGA AAA GAC TTC GCT TTC CCC CAG GAG ATG GTG GAG GGT GGC CAG CTC	144
	Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu	
40	35 40 45	
	CAG GAG GCC CAG GCC ATC TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC	192
	Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser	

	50	55	60	
	TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC			240
	Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr			
5	65	70	75	80
	CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG			288
	Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu			
	85	90	95	
10	GAT GCC TGC CTG GGG CAG GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA			336
	Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly			
	100	105	110	
15	AGA ACG GGC CCC ACC CTG GCC ATG AAG AGG TAT TTC CAG GGC ATC CAT			384
	Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His			
	115	120	125	
	GTC TAC CTG AAA GAG AAG GGA TAT AGT GAC TGC GCC TGG GAA ATT GTC			432
	Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val			
	130	135	140	
	AGA CTG GAA ATC ATG AGA TCC TTG TCT TCA TCA ACC AGC TTG CAC AAA			480
	Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys			
	145	150	155	160
	AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT			516
	Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro			
	165	170		
30				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg

1	5	10	15
Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp	20	25	30
5	Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu	35	40 45
10	Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser	50	55 60
Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	65	70	75 80
15	Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu	85	90 95
20	Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly	100	105 110
25	Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His	115	120 125
30	Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val	130	135 140
35	Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys	145	150 155 160
40	Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro	165	170